IN THE DRAWINGS

Please amend the drawings. Copies of figures with amendments in red ink are enclosed herewith.

REMARKS

The specification, claims, and drawings have been amended to comply add Sequence identification numbers in order to comply with sequence listing requirements.

It is respectfully submitted that no new matter has been introduced by the present amendments and entry of the same is respectfully requested.

CONCLUSION

Applicants believe all pending claims are now in condition for allowance and should be passed to issue. If the Examiner feels that a telephone conference would in any way expedite the prosecution of the application, please do not hesitate to call the undersigned at (408) 731-5875.

The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account 01-0431.
If the Examiner has any questions pertaining to this application, the Examiner is requested to contact the undersigned attorney.

Respectfully submitted,

Thomas Malone
Reg. No.: 40,078

Date: 1/24/03

VERSION WITH MARKINGS TO SHOW CHANGES MADE TO THE APPLICATION

In the Specification

Please amend the third paragraph on page 3 of specification as follows.

In one embodiment, the present invention provides an isolated growth factor polynucleotide comprising a nucleic acid sequence depicted in Figure 1B (SEQ ID NO: 02). In one aspect of this embodiment, the isolated polynucleotide comprising a nucleic acid sequence selected from the group consisting of: (a) a nucleic acid sequence of at least 90 nucleotides that is essentially identical to a linear sequence of comparable length contained in the sequence shown in Figure 1B (SEQ ID NO:02); (b) a nucleic acid sequence of at least 90 nucleotides encoding a polypeptide that is essentially identical to a linear sequence of at least 30 amino acids contained in the sequence shown in Figure 1A (SEQ ID NO:01); and (c) a complement of (a) or (b). In another aspect, the isolated polynucleotide encodes a polypeptide comprising an amino acid sequence that is essentially identical to a linear sequence of comparable length shown in Figure 1A (SEQ ID NO:01). In yet another aspect, the isolated polynucleotide encodes a polypeptide comprising an amino acid sequence essentially identical to the entire amino acid sequence shown in Figure 1A (SEQ ID NO:01). In still another aspect, the isolated polynucleotide encodes a polypeptide comprising the amino acid sequence shown in Figure 1A (SEQ ID NO:01). The polynucleotide of the present invention can code for the whole or domain(s) of the growth factor, or a mutant, fusion or a functionally equivalent growth factor polypeptide. In a related aspect of this embodiment, the invention encompasses a method of diagnosing a pathogenic condition or susceptibility to a pathogenic condition that is associated with a genetic alteration in a growth factor polypeptide encoded by the claimed polynucleotide. The method comprises the steps of: (a) providing a biological sample of a subject containing nucleic acid molecules and/or polypeptides; (b) determining a genetic alteration associated with the growth factor; and (c) correlating the alteration with a pathogenic condition or susceptibility to a pathogenic condition.

Please amend the first paragraph on page 4 of the specification as follows.

In another embodiment, the present invention includes a polynucleotide sequence that is useful as a probe for diagnostic or research purposes. Preferably, the probe is between 5 and 100 nucleotides in length and may comprise any of the contiguous nucleotides shown in Fig. 1A (SEQ ID NO:01). Longer sequences may be used as probes depending on the type of assay used.

Please amend page 6, line 21 of the specification as follows.

Figure 1A (SEQ ID NO:01) depicts the amino acid sequence for the peptide encoded by polynucleotide A.ctg12831-000000.10.0.

Please amend page 6, line 23 of the specification as follows.

Figure 1B (SEQ ID NO:02) depicts the polynucleotide sequence of A.ctg12831-000000.10.0.

Please amend the first paragraph on page 19 of the specfication as follows.

In a separate embodiment, the present invention provides an isolated polynucleotide comprising a nucleic acid sequence having at least about 90 nucleotides that is essentially identical to a linear sequence of comparable length contained in the sequence shown in 1B (SEQ ID NO:02). Preferably, the isolated polynucleotide contains at least about 90 nucleotide bases, more preferably at least about 150 nucleotides, more preferably at least about 450 nucleotides, and even more preferably at least about 1200 nucleotides. When the polynucleotide sequence is used as a probe, then it can also be shorter in length. For example, the sequence can be any contiguous nucleotides along the sequence shown in Fig. 1B (SEQ ID NO:02), its complement, or a variation of a few nucleotides. The length can be from 5, 13, 15, or 20 nucleotides to 25, 30, 50, 75, 100 or more nucleotides in length. In some embodiments very long sequences can be physically attached to a substrate that may be 500 to 5,000, or even 50,000 nucleotides long.

Please amend the second paragraph on page 19 of the specification as follows.

In another embodiment, the isolated polynucleotide comprises a nucleic acid sequence of at least 90 nucleotides that encodes a polypeptide essentially identical to a linear sequence of at least 30 amino acids depicted in Figure 1A (SEQ ID NO:01). Preferred linear peptide sequence is at least about 50 amino acids in length, more preferably at least 150 amino acids in length, and more preferably at least 350 amino acids. In yet another embodiment, the isolated polynucleotide may be any polynucleotide which encodes the polypeptide of Figure 1A (SEQ ID NO:01). In yet another embodiment, the isolated polynucleotide is a complement of any of the above mentioned growth factor polynucleotides.

Please amend the third paragraph on page 19 of the specification as follows.

These gene sequences can be identified, in whole or in part, by specifically hybridizing under moderate or stringent conditions to the exemplary polynucleotides shown in Figure 1B (SEQ ID NO:02). Alternatively, the invention sequences can be identified by their homology to published or known open reading frames, or pieces of genomic sequences using computer-assisted methods known in the art or those described herein.

Please amend the first paragraph on page 22 of the specification as follows.

Polynucleotides that correspond or align more closely to the exemplary sequences disclosed herein are comparably more preferred. A query polynucleotide of at least 90 nucleotides is considered to be essentially identical to a reference polynucleotide (e.g. sequences shown in 1B. (SEQ ID NO:02)), when the query polynucleotide exhibits at least about 80% sequence identity, more preferably at least about 90% identity, even more preferably at least about 95% identity using any of the above-mentioned alignment programs with the default settings. Likewise, a query polypeptide is essentially identical to a reference polypeptide of at least 30 amino acids, when the query polypeptide shares

at least 80% sequence identity, more preferably at least about 90% identity, even more preferably at least about 95% identity that can be discerned by the aforementioned programs using their respective default settings. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for example, 80% identical to a reference sequence of the present invention, the percentage of identity is preferably calculated over a linear sequence of comparable length that is contained in the reference sequence. Typically, the upper limit of gaps in homology is set at 20% of the total number of amino acid residues or nucleotide residues in the respective reference sequence. The altered residues may occur at the amino or carboxyl terminal positions of the reference sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence. Allowable sequence alterations include but are not limited to deletion, insertion, translocation and substitution of individual residues.

In the Claims

Please amend Claims 1, 2, 6, 7, 8 as follows:

1. An isolated polynucleotide comprising a nucleic acid sequence shown in Figure 1B (SEQ ID NO:02).

2. An isolated polynucleotide comprising a nucleic acid sequence selected from the group consisting of:

a) a nucleic acid sequence of at least 90 nucleotides that is essentially identical to a linear nucleotide sequence of comparable length depicted in Figure 1B (SEQ ID NO: 02);

b) a nucleic acid sequence of at least 90 nucleotides encoding a polypeptide that is essentially identical to a linear peptide sequence of at least 30 amino acids depicted in Figure 1A (SEQ ID NO:01); and

c) a complement of (a) or (b)

6. The isolated polynucleotide of claim 2 wherein said nucleic acid encodes a polypeptide - comprising an amino acid sequence that is essentially identical to a linear sequence of comparable length shown in Figure 1A (SEQ ID NO:01).

7. The isolated polynucleotide of claim 2 wherein said nucleic acid sequence encodes a polypeptide comprising the amino acid sequence shown in Figure 1A (SEQ ID NO:01)

8. The isolated polynucleotide of claim 2 wherein said nucleic acid encodes a polypeptide comprising an amino acid sequence essentially identical to the entire amino acid sequence shown in Figure 1A (SEQ ID NO:01).

Figure 1

Sequence Name:

A.ctg12831-000000.10.0

Figure 1A: SEQ ID NO: 01

MGKDFMSKTPKAMATKAKIDKWDLIKLKSFCTAKETTIRVNRQLTEWEKIFATYSFDKGL
ISRIYNELKQIYKKKTKNPIKKWVKDMNRHFSKEGIYAAKKHMKKYSSSLAIREMQIKTT
MRYHLTPVRMAIIKKSGNNRDMDEAGNHHSQQTITRTKNQTPHVLTHRWILQQSHWVTVL
SDISELMHKTDRIVNLLMCMYLLTVDLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFF
PRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQ
LDHHERCDCICSSRPPR

Figure 1B: SEQ ID NO: 02

GTATATGTAAGAAAGCCTCATCTTTTGATTTTTAATATACAAGATGCTTTCTTTAAGAGA
GCAAGATTCAAAATTGTTTTGTGTTTCAAAATTTAAAAATAAATTTATCTCCTAAATTTT
CTAAAGACATGTTTCATATATTTGACCATCCCTTATTTTGGCAAAGGATTTTAAGAGTCT
AACTCAAACATATGTAAGCTCTGGTGTACCTGGTTATATATACCAAAAAAAACATTTGAT
CTATATACACATAGACATGAATATATTTCTGTGTGTGTTTGTGCATATATAACCTCAAAC
ACTATTATTAAATGCAATCCTATATTCTTAGGTATAGAAGTTGATGATATACCTTTCTAC
TTGCCATGGCATTAACAAAGCAAGGCTGAGACTCAGCAACCACTTGTGTTCATTGCATTG
CAGGCTAGTAGTAAGTTTGGTTGCTGGTAGGAAAAGGGTCTCTTATCTCACCCTCCTTAA
ACTAAAGGTTCTTTCAGGCTTAATGTAAGGATGTGCACATTCTCTTATCGAGGTGGTCTT
GAGCTGCAGATACAATCACATCGTTCATGGTGATCCAACTGGATGTCAACTAGAGCCATG
GTCTTAGCTCTACCCCTCCTCTTGATGTGGCCAGGCTCAAACTGTAATACCTAGGACAAG
AAGCACATCTCCTGTTAGAAAGCCTTTGGAGTTCAACTCAGTCAGATGCCACCTACTTAT
TACCTTTTTGACAACTAGTTCTTAGCCCTTTGAGAACCCAACAGAAGCTATGGGCTTGCT
ATTAGAATGCACACGTTGCTATTAGAATGTACACATTTTTCAAATAATTGACTCCCTGAA
GTGGAGGAATCAATTGATCCCAGAGTAATGCCCAGCATAACTTACCTGAAGTACCCAGAT
GATTTCATGTGTCTTAGCAGGTATTTATTAATAGCTTTCTAAGGGCCTGCTTTGGGCCAA
GTACTGTTCCAAATATTATCGTAAAGATCCTTCTGACCAAGGCATGTGTTATAGATGAAT
ACAATACTTGAGCATATTATTAGCATGGAGAGGAAAATGAATACAACCATGAATAAAATA
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ATGGCCGAACAGGAACAGCTCTGGTCTGCAGTTCCCAGCGAGATCAATGCAGAAGGCGGG
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GGTGCAGCCCACGGAAGGTGAGCTGAAGCAGGGTGGGGTGTCCCCTCAGCCGCGAAGTGC
AAGGGGGTGGGGGATCTCCTTCCCCCAGCCAAGGGAAGCCATGAGAGACTGTACCAGGAG
GAATGGTGCACTCTAGTCCAGATACTGCACTTTTCCCATAGTCTTTGCAACTGGCAGACC
AGGAGATTTCCCCCAGTGCCTATGCCACCAGGGCCCTGGGTTTCAAGCACAAAACTGGGC
GGCCATTTGGACAGACACCGAGCTAGCCGCAGCAGTTTATTTTTCATACCCCAGTGGCGC
CTGGAATGCCAGCAAGACAGAACCATTCACTCCAGGGATCCAAGTGGTCTGGCTCAGTGG
GTCCCACCCCCATGGAGCCCAGCTAGCTAAGATCCACTGGCTTGAAATTCTCCTGCCAGC
ACAGCAGTCTGAGATTGACCTGGGATGCTTGAGCTTGGTGAGGGGAGGGGCGTCTGCCAT
TGCTGAGGCTTGAGTAGGCGAGGCGGTTTTACCCTCAAAGTGTAAACAAAGCTACTGGGA
AGTTTGAATGGGGCGCCCACCGCAGCTCAGCAAGGCCGCTGTGGCAAACTGCCTCTCTAG
ATTCCTCCTTTTTGGGCAGGTCATCTCTGAAAGAAAGGCAGCAGCCCCAGTCAGGGACTT
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CAGCTTCTCAGACTTAAACATTCCTGCCTGGAGGCTCTGAAGAGAGCAGCGGATCTCCCA
GCACAGCATTTGAGCTCTGATAAGGGACAGGCTGCCTCCTCAAGTGGGTCCCTGACCCCC
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AGGGTCTGGAGTGGACCTCCAGCAAACTCCAGCAGACCTGCAGCAGAGCGGCCTGACTGT
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ATGGGAAAAACCAGTGCAGAAACACTGAAAATTCCAAAAACCAGAACTCCTCTTCTCAAC
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CTCCCACACAATAATAGTGGGAGTCTAAATAATAAATAGACACTTTAACACCCCACTGCC
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AGAAAACATAATGGAAAGCCTGGGTGGGCACTACATTTCAGAGCATGGCATTAGCATTGG
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GAACTTTAAAGTAGTTTTTTCCAATTCTGTGAAGAAAGTAA